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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2010; month=2; day=19; hr=9; min=42; sec=47; ms=323;]

=====

Reviewer Comments:

1.

E355 Empty lines found between the amino acid numbering and
the proteins SEQID (11)

E321 No. of Bases conflict, this line has no nucleotides
SEQID (11) POS (126)

E355 Empty lines found between the amino acid numbering and
the proteins SEQID (12)

E321 No. of Bases conflict, this line has no nucleotides
SEQID (12) POS (0)

E355 Empty lines found between the amino acid numbering and
the proteins SEQID (12)

E321 No. of Bases conflict, this line has no nucleotides
SEQID (12) POS (512)

E355 Empty lines found between the amino acid numbering and
the proteins SEQID (22)

E321 No. of Bases conflict, this line has no nucleotides
SEQID (22) POS (112)

E355 Empty lines found between the amino acid numbering and
the proteins SEQID (24)

E321 No. of Bases conflict, this line has no nucleotides
SEQID (24) POS (496)

E355 Empty lines found between the amino acid numbering and
the proteins SEQID (28)

E321 No. of Bases conflict, this line has no nucleotides
SEQID (28) POS (16)

E355 Empty lines found between the amino acid numbering and
the proteins SEQID (30)

E321 No. of Bases conflict, this line has no nucleotides
SEQID (30) POS (48)

<210> 11
 <211> 1582
 <212> DNA
 <213> Zea mays
 <220>
 <221> CDS
 <222> (10)..(1563)
 <223> Shrunk-2 gene revertant form
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 <221> variation
 <222> (267)
 <223> k = g or t; amino acid 86 = Ala.
 <220>
 <221> variation
 <222> (1368)
 <223> r = a or g; amino acid 453 = Pro.
 <220>
 <221> variation
 <222> (1578)
 <223> k = g or t.
 * * * * *

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc	387
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115 120 125	

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act	435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr	
130 135 140	

tgc ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac	483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn	
145 150 155	

For SEQ ID # 11, 12, 22, 24, 28, and 30 the sequence rules specify the numbering for amino acids be placed below the line of amino acids in a protein or coding region of a nucleotide sequence.

"Sec. 1.822 Symbols and format to be used for nucleotide and/or amino acid sequence data.

(a) The symbols and format to be used for nucleotide and/or amino

acid sequence data shall conform to the requirements of paragraphs (b) through (e) of this section.

(d) Representation of amino acids. (1) The amino acids in a protein or peptide sequence shall be listed using the three-letter abbreviation with the first letter as an upper case character, as in WIPO Standard ST.25 (1998), Appendix 2, Table 3.

(4) The enumeration of amino acids may start at the first amino acid of the first mature protein, with the number 1. When presented, the amino acids preceding the mature protein, e.g., pre-sequences, pro-sequences, pre-pro-sequences and signal sequences, shall have negative numbers, counting backwards starting with the amino acid next to number 1. Otherwise, the enumeration of amino acids shall start at the first amino acid at the amino terminal as number 1. It shall be marked below the sequence every 5 amino acids."

In the SEQ ID numbers listed above there are blank lines found between the amino acids and the numbering for the amino acids at different locations. Please remove all blank lines found between the amino acids and the numbering in these sequences.

2.

E300	Invalid codon found Asn SEQID (11) POS: 388
E300	Invalid codon found Ser SEQID (11) POS: 391
E300	Invalid codon found Gly SEQID (11) POS: 394
E300	Invalid codon found Ile SEQID (11) POS: 397
E300	Invalid codon found Asn SEQID (11) POS: 400
E300	Invalid codon found Lys SEQID (11) POS: 403
E300	Invalid codon found Ile SEQID (11) POS: 406
E300	Invalid codon found Phe SEQID (11) POS: 409
E300	Invalid codon found Val SEQID (11) POS: 412
E300	Invalid codon found Met SEQID (11) POS: 415
E300	Invalid codon found Ser SEQID (11) POS: 418
E300	Invalid codon found Gln SEQID (11) POS: 421
E300	Invalid codon found Phe SEQID (11) POS: 424
E300	Invalid codon found Asn SEQID (11) POS: 427
E300	Invalid codon found Ser SEQID (11) POS: 430
E300	Invalid codon found Thr SEQID (11) POS: 433

The errors shown above are ok and require no response.

Application No: 10569000 Version No: 1.0

Input Set:**Output Set:**

Started: 2010-02-18 13:09:42.494
Finished: 2010-02-18 13:09:51.451
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 957 ms
Total Warnings: 0
Total Errors: 302
No. of SeqIDs Defined: 42
Actual SeqID Count: 42

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 300	Invalid codon found Asn SEQID (11) POS: 388
E 300	Invalid codon found Ser SEQID (11) POS: 391
E 300	Invalid codon found Gly SEQID (11) POS: 394
E 300	Invalid codon found Ile SEQID (11) POS: 397
E 300	Invalid codon found Asn SEQID (11) POS: 400
E 300	Invalid codon found Lys SEQID (11) POS: 403
E 300	Invalid codon found Ile SEQID (11) POS: 406
E 300	Invalid codon found Phe SEQID (11) POS: 409
E 300	Invalid codon found Val SEQID (11) POS: 412
E 300	Invalid codon found Met SEQID (11) POS: 415
E 300	Invalid codon found Ser SEQID (11) POS: 418
E 300	Invalid codon found Gln SEQID (11) POS: 421
E 300	Invalid codon found Phe SEQID (11) POS: 424
E 300	Invalid codon found Asn SEQID (11) POS: 427
E 300	Invalid codon found Ser SEQID (11) POS: 430
E 300	Invalid codon found Thr SEQID (11) POS: 433
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (12)

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (12)
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna This error has occurred more than 20 times, will not be displayed

Input Set:

Output Set:

Started: 2010-02-18 13:09:42.494
Finished: 2010-02-18 13:09:51.451
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 957 ms
Total Warnings: 0
Total Errors: 302
No. of SeqIDs Defined: 42
Actual SeqID Count: 42

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (22)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (24)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (28)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (30)

SEQUENCE LISTING

<110> University of Florida Research Foundation, Inc.
Hannah, L. Curtis
Lyerly Linebarger, Carla R.

<120> Heat Stable Variants of Adenosine Diphosphate Glucose Pyrophosphorylase

<130> UF-371XC1 PCT

<140> 10569000

<141> 2010-02-18

<150> US 60/496,188

<151> 2003-08-18

<160> 42

<170> PatentIn version 3.2

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<211> 1425

<212> DNA

<213> zea mays

<400> 1

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attcctgtca gcaattgtct caacagcaac atatccaaga tctatgtgct aacgcaattt	300
aactctgctt cccccaaccg tcacctctca agagcctacg ggagcaacat tggagggtac	360
aagaatgaag ggtttgttga agtcttagct gcacagcaga gccagataa tccaaactgg	420
tttcagggtg ctgcagatgc tgtaaggcag tacttgttgt tgtttgagga gcataatgtg	480
atggaatttc taattcttgc tggcgatcac ctgtaccgga tggactatga aaagttcatt	540
caggcacaca gagaacaaaa tgctgatatt accgttgctg ccctaccgat ggatgagaaa	600
cgtgcaactg catttggcct catgaaaatt gatgaagaag ggaggatcat tgagtttgct	660
gagaaaccga aaggagagca gttgaaagca atgatggttg acaccacat acttggcctt	720
gatgacgtga gggcaaagga aatgccttat attgctagca tgggtatcta tgttttcagc	780
aaagatgtaa tgcttcagct cctccgtgaa caatttcctg aagccaatga ctttgggaagt	840
gaggttattc cagggtgcaac cagcattgga aagagggttc aggttatct gtatgatggt	900
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gtcacagtga tcaaggatgc tttactccct agtggacag ttata 1425

<210> 2
<211> 475
<212> PRT
<213> zea mays

<400> 2

Met Asp Met Ala Leu Ala Ser Lys Ala Ser Pro Pro Pro Trp Asn Ala
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Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
20 25 30

Asp Ser Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile
35 40 45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
50 55 60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
65 70 75 80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
85 90 95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
100 105 110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
115 120 125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
130 135 140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
145 150 155 160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
165 170 175

Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val			
180	185	190	
Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met			
195	200	205	
Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys			
210	215	220	
Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu			
225	230	235	240
Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile			
245	250	255	
Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe			
260	265	270	
Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser			
275	280	285	
Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp			
290	295	300	
Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys			
305	310	315	320
Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr			
325	330	335	
Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val			
340	345	350	
Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile			
355	360	365	
Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile			
370	375	380	
Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala			
385	390	395	400
Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly			
405	410	415	
Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile			
420	425	430	
Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala			
435	440	445	
Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val Ile			
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Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile			
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<211> 1425

<212> DNA

<213> zea mays

<400> 3

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ttgacaaaaga agcgtgccaa gcttgcagtg ccattgggtg ccaactatag actgattgat      240
attcctgtca gcaattgtct caacagcaac atatccaaga tctatgtgct aacgcaattt      300
aactctgctt cccccaaccg tcacctctca agagcctacg ggagcaacat tggagggtag      360
aagaatgaag ggtttgttga agtcttagct gcacagcaga gccagataa tccaaactgg      420
tttcagggtg ctgcagatgc tgtaaggcag tacttgtggt tgtttgagga gcataatgtg      480
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caggcacaca gagaacaaaa tgctgatatt accgttgctg ccctaccgat ggatgagaaa      600
cgtgcaactg catttggcct catgaaaatt gatgaagaag ggaggatcat tgagtttgc      660
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cacctgccac cttcaaaggt tcttgatgct gatgtgacag acagtgttat tggggaagga     1080
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gataaaaaac tccttgccga aaaaggtggc attcctattg gtattgggaa aaattcatgc     1260
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<212> PRT
<213> zea mays

<400> 4

Met Asp Met Ala Leu Ala Ser Lys Ala Ser Pro Pro Pro Trp Asn Ala
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Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
20 25 30

Asp Ser Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile
35 40 45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
50 55 60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
65 70 75 80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
85 90 95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
100 105 110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
115 120 125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
130 135 140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
145 150 155 160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
165 170 175

Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val
180 185 190

Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met
195 200 205

Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys
210 215 220

Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu
225 230 235 240

Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile
245 250 255

Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe
 260 265 270

Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser
 275 280 285

Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp
 290 295 300

Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys
 305 310 315 320

Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr
 325 330 335

Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val
 340 345 350

Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile
 355 360 365

Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile
 370 375 380

Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala
 385 390 395 400

Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly
 405 410 415

Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile
 420 425 430

Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala
 435 440 445

Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val Ile
 450 455 460

Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
 465 470 475

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 <213> zea mays

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<212> PRT
<213> zea mays

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50		55		60
Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile				
65		70		80
Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr				
	85		90	95
Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg				
	100		105	110
Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu				
	115		120	125
Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly				
	130		135	140
Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn				
145		150		155
Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp				
	165		170	175
Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr				
	180		185	190
Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu				
	195		200	205
Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro				
	210		215	220
Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly				
225		230		235
Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly				
	245		250	255
Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln				
	260		265	270
Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr				
	275		280	285
Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu				
	290		295	300
Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr				
305		310		315
Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile				
	325		330	335
Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp				

340

345

350

Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys
355 360 365

Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala
370 375 380

Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu
385 390 395 400

Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile
405 410 415

Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg
420